



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/927,734  
Source: OIPE  
Date Processed by STIC: 08/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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## Raw Sequence Listing Error Summary

### ERROR DETECTED    SUGGESTED CORRECTION

SERIAL NUMBER: 09/927,734

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos:    was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                              prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering                use space characters, instead.
  
- 4      Non-ASCII            The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
                              ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
                              each n or Xaa can only represent a single residue. Please present the maximum number of each  
                              residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0        A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                    sequences(s)         . Normally, PatentIn would automatically generate this section from the  
                              previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                              the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
                              Artificial or Unknown sequences.
  
- 7      Skipped Sequences    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                              (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                              (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                              This sequence is intentionally skipped  
  
                              Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)            <210> sequence id number  
                              <400> sequence id number  
                              000
  
- 9 ✓      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)            Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                              In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>        Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response                scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                              is Artificial Sequence
  
- 11      Use of <220>        Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                              Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                              "Unknown." Please explain source of genetic material in <220> to <223> section.  
                              (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0        Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                              listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

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OIPE

## RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/927,734C

TIME: 16:02:58

Input Set : A:\06279-1.txt

Output Set: N:\CRF3\08162001\I927734.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Selitrennikoff, Claude  
 4 Nakata, Mitsunori  
 6 <120> TITLE OF INVENTION: Method for the Identification of Fungal Glucose Utilization  
 7 Inhibitors and Antifungal Agents  
 9 <130> FILE REFERENCE: MYCOLOGX-06279  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/927,734  
 C--> 11 <141> CURRENT FILING DATE: 2001-08-10  
 11 <160> NUMBER OF SEQ ID NOS: 14  
 13 <170> SOFTWARE: PatentIn version 3.0  
 15 <210> SEQ ID NO: 1  
 16 <211> LENGTH: 20  
 17 <212> TYPE: PRT  
 18 <213> ORGANISM: Artificial Sequence ✓  
 20 <220> FEATURE:  
 21 <223> OTHER INFORMATION: Synthetic ✓  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: SITE  
 25 <222> LOCATION: (1)..(1)  
 26 <223> OTHER INFORMATION: Xaa at this position can be Val, Ile, or Leu.  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: SITE  
 31 <222> LOCATION: (4)..(6)  
 32 <223> OTHER INFORMATION: Xaa at these positions can be Val, Ile, or Leu.  
 35 <220> FEATURE:  
 36 <221> NAME/KEY: SITE  
 37 <222> LOCATION: (7)..(9)  
 38 <223> OTHER INFORMATION: Xaa at these positions can be any amino acid.  
 41 <220> FEATURE:  
 42 <221> NAME/KEY: SITE  
 43 <222> LOCATION: (10)..(10)  
 44 <223> OTHER INFORMATION: Xaa at this position can be Val, Ile, or Leu.  
 47 <220> FEATURE:  
 48 <221> NAME/KEY: SITE  
 49 <222> LOCATION: (13)..(13)  
 50 <223> OTHER INFORMATION: Xaa at this position can be any amino acid.  
 53 <220> FEATURE:  
 54 <221> NAME/KEY: SITE  
 55 <222> LOCATION: (15)..(15)  
 56 <223> OTHER INFORMATION: Xaa at this position can be Val, Ile, or Leu.  
 59 <220> FEATURE:  
 60 <221> NAME/KEY: SITE  
 61 <222> LOCATION: (17)..(17)  
 62 <223> OTHER INFORMATION: Xaa at this position can be Ser or Thr.  
 65 <220> FEATURE:  
 66 <221> NAME/KEY: SITE  
 67 <222> LOCATION: (18)..(18)  
 68 <223> OTHER INFORMATION: Xaa at this position can be any amino acid.

Does Not Comply  
Corrected Diskette Needed

See page 2 of 6

DATE: 08/23/2001  
TIME: 16:02:58

Input Set : A:\06279-1.txt  
Output Set: N:\CRF3\08162001\I927734.raw

71 <220> FEATURE:  
72 <221> NAME/KEY: SITE  
73 <222> LOCATION: (19)..(20)  
74 <223> OTHER INFORMATION: Xaa at these positions can be Val, Ile, or Leu.  
77 <400> SEQUENCE: 1 ✓✓✓✓✓✓✓✓  
W--> 79 Xaa Glu Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Gly Xaa Gly Xaa Gly  
80 1 5 10 15  
W--> 82 Xaa Xaa Xaa Xaa  
83 20  
85 <210> SEQ ID NO: 2  
86 <211> LENGTH: 13  
87 <212> TYPE: PRT  
88 <213> ORGANISM: Artificial Sequence ✓  
90 <220> FEATURE:  
91 <223> OTHER INFORMATION: Synthetic ✓  
93 <220> FEATURE:  
94 <221> NAME/KEY: SITE  
95 <222> LOCATION: (2)..(2)  
96 <223> OTHER INFORMATION: Xaa at this position can be any amino acid.  
99 <220> FEATURE:  
100 <221> NAME/KEY: SITE  
101 <222> LOCATION: (5)..(5)  
102 <223> OTHER INFORMATION: Xaa at this position can be Val, Ile, or Leu.  
105 <220> FEATURE:  
106 <221> NAME/KEY: SITE  
107 <222> LOCATION: (6)..(6)  
108 <223> OTHER INFORMATION: Xaa at this position can be any amino acid.  
111 <220> FEATURE:  
112 <221> NAME/KEY: SITE  
113 <222> LOCATION: (7)..(7)  
114 <223> OTHER INFORMATION: Xaa at this position can be Val, Ile, or Leu.  
117 <220> FEATURE:  
118 <221> NAME/KEY: SITE  
119 <222> LOCATION: (9)..(9)  
120 <223> OTHER INFORMATION: Xaa at this position can be any amino acid.  
123 <220> FEATURE:  
124 <221> NAME/KEY: SITE  
125 <222> LOCATION: (10)..(10)  
126 <223> OTHER INFORMATION: Xaa at this position can be Lys, Arg, or His.  
129 <220> FEATURE:  
130 <221> NAME/KEY: SITE  
131 <222> LOCATION: (11)..(11)  
132 <223> OTHER INFORMATION: Xaa at this position can be Val, Ile, or Leu.  
135 <220> FEATURE:  
136 <221> NAME/KEY: SITE  
137 <222> LOCATION: (12)..(12) Errored - change to (13)..(13)  
138 <223> OTHER INFORMATION: Xaa at this position can be Tyr or Phe..  
141 <400> SEQUENCE: 2  
W--> 143 Asn Xaa Pro Ala Xaa Xaa Xaa Tyr Xaa Xaa Xaa Gly Xaa

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Sequence location does not match sequence.

## RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/927,734C

TIME: 16:02:58

Input Set : A:\06279-1.txt

Output Set: N:\CRF3\08162001\I927734.raw

144 1 5 10  
146 <210> SEQ ID NO: 3  
147 <211> LENGTH: 20  
148 <212> TYPE: PRT  
149 <213> ORGANISM: Candida albicans  
151 <400> SEQUENCE: 3  
153 Ile Glu Asp Ile Ser Val Ala Lys Ser Glu Gln Gly Lys Lys Leu Gly  
154 1 5 10 15  
156 Tyr Tyr Leu Val  
157 20  
159 <210> SEQ ID NO: 4  
160 <211> LENGTH: 10  
161 <212> TYPE: PRT  
162 <213> ORGANISM: Candida albicans  
164 <400> SEQUENCE: 4  
166 Asn Val Gly Phe Tyr Glu Lys Cys Gly Tyr  
167 1 5 10  
169 <210> SEQ ID NO: 5  
170 <211> LENGTH: 23  
171 <212> TYPE: PRT  
172 <213> ORGANISM: Saccharomyces cerevisiae  
174 <400> SEQUENCE: 5  
176 Ile Glu Asp Ile Ala Val Asn Ser Lys Tyr Gln Gly Gln Gly Leu Gly  
177 1 5 10 15  
179 Lys Leu Leu Ile Pro Arg Thr  
180 20  
182 <210> SEQ ID NO: 6  
183 <211> LENGTH: 10  
184 <212> TYPE: PRT  
185 <213> ORGANISM: Saccharomyces cerevisiae  
187 <400> SEQUENCE: 6  
189 Asn Val Lys Phe Tyr Glu Lys Cys Gly Phe  
190 1 5 10  
192 <210> SEQ ID NO: 7  
193 <211> LENGTH: 20  
194 <212> TYPE: PRT  
195 <213> ORGANISM: Mus musculus  
197 <400> SEQUENCE: 7  
199 Val Glu Asp Val Val Val Ser Asp Glu Cys Arg Gly Lys Gln Leu Gly  
200 1 5 10 15  
202 Lys Leu Leu Leu  
203 20  
205 <210> SEQ ID NO: 8  
206 <211> LENGTH: 10  
207 <212> TYPE: PRT  
208 <213> ORGANISM: Mus musculus  
210 <400> SEQUENCE: 8  
212 Asn Val Gly Phe Tyr Lys Lys Phe Asp Tyr  
213 1 5 10

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/927,734C

DATE: 08/23/2001

TIME: 16:02:58

Input Set : A:\06279-1.txt

Output Set: N:\CRF3\08162001\I927734.raw

215 <210> SEQ ID NO: 9  
216 <211> LENGTH: 20  
217 <212> TYPE: PRT  
218 <213> ORGANISM: Homo sapiens  
220 <400> SEQUENCE: 9  
222 Leu Glu Asp Phe Phe Val Met Ser Asp Tyr Arg Gly Phe Gly Ile Gly  
223 1 5 10 15  
225 Ser Glu Ile Leu  
226 20  
228 <210> SEQ ID NO: 10  
229 <211> LENGTH: 13  
230 <212> TYPE: PRT  
231 <213> ORGANISM: Homo sapiens  
233 <400> SEQUENCE: 10  
235 Asn Glu Pro Ser Ile Asn Phe Tyr Lys Arg Arg Gly Ala  
236 1 5 10  
238 <210> SEQ ID NO: 11  
239 <211> LENGTH: 20  
240 <212> TYPE: PRT  
241 <213> ORGANISM: Homo sapiens  
243 <400> SEQUENCE: 11  
245 Tyr Ser Thr Gly Met Val His Leu Leu Leu Gln Val Thr Ile Asp Gly  
246 1 5 10 15  
248 Arg Asn Tyr Ile  
249 20  
251 <210> SEQ ID NO: 12  
252 <211> LENGTH: 10  
253 <212> TYPE: PRT  
254 <213> ORGANISM: Homo sapiens  
256 <400> SEQUENCE: 12  
258 Ile Glu Ala Tyr Phe Glu Arg Ile Gly Tyr  
259 1 5 10  
261 <210> SEQ ID NO: 13  
262 <211> LENGTH: 20  
263 <212> TYPE: PRT  
264 <213> ORGANISM: Homo sapiens  
266 <400> SEQUENCE: 13  
268 Leu Phe His Leu Ser Val Asp Asn Glu His Arg Gly Gln Gly Ile Ala  
269 1 5 10 15  
271 Lys Ala Leu Val  
272 20  
274 <210> SEQ ID NO: 14  
275 <211> LENGTH: 13  
276 <212> TYPE: PRT  
277 <213> ORGANISM: Homo sapiens  
279 <400> SEQUENCE: 14  
281 Gln Leu Ser Ala Met Gly Leu Tyr Gln Ser Leu Gly Phe  
282 1 5 10

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/927,734C

DATE: 08/23/2001

TIME: 16:02:59

Input Set : A:\06279-1.txt

Output Set: N:\CRF3\08162001\I927734.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

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